Paper No. 36

UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE BOARD OF PATENT APPEALS AND INTERFERENCES

Ex parte OLGA BANDMAN, JENNIFER L. HILLMAN,
PREETI LAL, KARL J. GUEGLER,
GINA GORGONE, NEIL C. CORLEY,
CHANDRA PATTERSON, and
MARIAH R. BAUGHN

Appeal No. 2003-1805
Application No. 09/079,892

ON BRIEF

Before WINTERS, WILLIAM F. SMITH, and GRIMES, Administrative Patent Judges.

WILLIAM F. SMITH, Administrative Patent Judge.

DECISION ON APPEAL

This is an appeal under 35 U.S.C. § 134 from the final rejection of claims 25 through 28 and 33 through 37. Claims 6 through 12 are pending and have been allowed. Claims 29 through 32 are also pending but have been withdrawn from consideration by the examiner. Claims 25 and 33 are representative of the subject matter on appeal. Since claim 25 refers to allowed claim 7, we reproduce claims 7, 25, and 33 as follows:

7. An isolated and purified polynucleotide comprising a polynucleotide sequence as shown in SEQ ID NO:4, wherein said polynucleotide of SEQ ID NO:4 encodes a polypeptide having glutamine fructose-6-phosphate amidotransferase activity.

25. A method for detecting a target polynucleotide in a sample, wherein said target polynucleotide comprises the polynucleotide of claim 7, the method comprising:

a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and

b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

33. An isolated polynucleotide selected from the group consisting of:

a) a polynucleotide comprising the polynucleotide sequence of SEQ ID NO:4,

b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to the polynucleotide sequence of SEQ ID NO:4,

c) a polynucleotide complementary to a polynucleotide of a),

d) a polynucleotide complementary to a polynucleotide of b), and

e) an RNA equivalent of a)-d).

The examiner relies upon the following references:

Nishi et al. (Nishi ‘713)	5,876,713	Mar. 2, 1999
Eur. Pat. App. (Nishi EPA)	EP 824,149 A2	Feb. 18, 1998

Claims 33 through 37 stand rejected under 35 U.S.C. § 112, first paragraph (written description). Claims 25 through 28 and 37 stand rejected under 35 U.S.C. § 103(a). As evidence of obviousness, the examiner relies upon Nishi ‘713 and Nishi EPA in the alternative. We reverse the written description rejection and affirm the obviousness rejection.

Background

The present invention involves human carbohydrate metabolism enzymes referred to by appellants as "CARM." Specification, page 5. As seen from claims 7, 25, and 33 reproduced above, the claims under review in this appeal involve the polynucleotide sequence as shown in SEQ ID NO:4 which is said to code for CARM-1. Id., page 19, lines 14 through 20. As explained:

> CARM-1 has chemical and structural similarity with human glutamine: fructose-6-phosphate amidotransferase (GI 183082). In particular, CARM-1 and human glutamine: fructose-6-phosphate amidotransferase share 78% identity. A fragment of SEQ ID NO:4 from about nucleotide 243 to about nucleotide 260 is useful, for example, as a hybridization probe. Northern analysis shows the expression of this sequence in various libraries, at least 51% of which are immortalized or cancerous and at least 46% of which involve immune response. Of particular note is the expression of CARM-1 in gastrointestinal, male and female reproductive, and nervous tissues.

Id., page 20, lines 4 through 11.

Discussion

1. Written description.

The examiner considers that claims 33 through 37 do not comply with the written description requirement of 35 U.S.C. § 112, first paragraph, since:

> The specification defines an 'allelic sequence' (see page 10) as an alternative form of the gene which may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered and that any given natural or recombinant gene may have none, one or many, allelic forms, and that common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, substitutions of nucleotides each of which may occur alone or in combination with the others one or more times in a given sequence. This definition does not provide any specific information about the structure of naturally occurring (alleles) variants of SEQ ID NO:4 (i.e. where are the regions within which mutations are likely to occur) nor discloses any function for naturally occurring variants. There is no description of the mutational sites that exist in nature, and there is no description of how the structure of SEQ ID NO:4 relates to the structure of any naturally

> occurring alleles. The general knowledge in the art concerning alleles does not provide any indication of how one allele is representative of unknown alleles. The nature of alleles is such that they are variant structures, and in the present state of the art structure of one does not provide guidance to the structure of others. Therefore, many functionally unrelated DNAs are encompassed within the scope of these claims. The specification discloses only a single species of the claimed genus (i.e. the sequence encoding SEQ ID NO:2) which is insufficient to put one of skill in the art in possession of the attributes and features of all species within the claimed genus. Therefore, one skilled in the art cannot reasonably conclude that the applicant had possession of the claimed invention at the time the instant application was filed.

Examiner's Answer, paragraph bridging pages 3 and 4.

The examiner also

> [F]ully acknowledges appellants' recitation of the structural limitations of the polynucleotides of claim 33 parts b) and d)-e). However, the polynucleotides as defined in claim 33 parts b) and d)-e) encompass a genus of polynucleotides that encompasses widely variant species, some having the same functions as the polypeptide of SEQ ID NO:1, some having unknown and distinctly different functions and some possibly having no function. While one of skill in the art, provided the polynucleotide sequence of SEQ ID NO:4, may be able to recognize variants of SEQ ID NO:4 with nucleotide sequence sharing 90% identity, one cannot recognize which of these variants occurs naturally and is thus encompassed by the genus of claim 33 part b). Therefore, the skilled artisan would not be able to recognize a member of the claimed genus of polynucleotides merely from its structural definition. This enormous genus will encompass a wide variety of polynucleotides with their own distinct properties. Because appellants have provided no functional limitation for the claimed polynucleotides, the single disclosed polynucleotide of SEQ NO:4 is not representative of the entire genus and one of skill in the art would not recognize that appellants were in possession of all polynucleotides comprising a naturally-occurring polynucleotide having at least 90% identity to SEQ ID NO:4 as encompassed by the claims.

Examiner's Answer, paragraph bridging pages 11 and 12.

The Federal Circuit discussed the application of the written description requirement to inventions in the field of biotechnology in University of California v. Eli Lilly and Co., 119 F.3d 1559, 1568, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997), stating

that "[a] written description of an invention involving a chemical genus, like a description of a chemical species, 'requires a precise definition, such as by structure, formula, [or] chemical name,' of the claimed subject matter sufficient to distinguish it from other materials" Id. at 1567, 43 USPQ2d at 1405. The court also stated that

> a generic statement such as 'vertebrate insulin cDNA' or 'mammalian insulin cDNA,' without more, is not an adequate written description of the genus because it does not distinguish the genus from others, except by function. It does not specifically define any of the genes that fall within its definition. It does not define any structural features commonly possessed by members of the genus that distinguish them from others. One skilled in the art therefore cannot, as one can do with a fully described genus, visualize or recognize the identity of the members of the genus. A definition by function, as we have previously indicated, does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is.

Id. at 1568, 43 USPQ2d at 1406. The court concluded that "naming a type of material generally known to exist, in the absence of knowledge as to what that material consists of, is not a description of that material." Id.

Finally, the court addressed the manner by which a genus of cDNAs might be described. "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus." Id.

In reviewing this rejection, we note that the examiner has not rejected claim 8 under this section of the statute. Claim 8 reads:

8. An isolated and purified polynucleotide comprising a naturally occurring polynucleotide sequence having at least 90% sequence identity to the polynucleotide of SEQ ID NO:4, wherein said naturally occurring polynucleotide sequence encodes a polypeptide having glutamine-fructose-6-phosphate amidotransferase activity.

As seen, claim 8 differs from claim 33 b) which is the focus of the examiner's written description rejection in that it adds the limitation that the naturally occurring polynucleotide sequence encodes a polypeptide having glutamine-fructose-6-phosphate amidotransferase activity. Since the examiner has conceded that a claim having the scope of claim 8 complies with the written description requirement of 35 U.S.C. § 112, we do not find that the lack of a statement of function in claim 33 b) means that that portion of the claim lacks written descriptive support.

Claim 33 b) defines a genus of polynucleotides by way of two significant qualifiers. First, the polynucleotide of claim 33 b) must be "naturally occurring." Second, the polynucleotide of claim 33 b) must be "at least 90% identical to the polynucleotide sequence of SEQ ID NO:4." As explained in Lilly, a genus of polynucleotides can be described by a representative number of polynucleotides sharing common structural features which constitute a substantial portion of the genus. The examiner is correct in his analysis that claim 33 b) includes so-called nonfunctional alleles. However, those nonfunctional alleles must be "naturally occurring" and be at least "90% identical to the polynucleotide sequence of SEQ ID NO:4." In our view, these two limitations adequately describe the genus of polynucleotides encompassed by claim 33 b) without that claim further including a functional limitation.

We understand the examiner's concern that one may not recognize that a polynucleotide sequence having 90% identity with that of SEQ ID NO: 4 is "naturally occurring." However, that concern is more properly raised under a rejection under 35 U.S.C. § 112, second paragraph, rather than the written description requirement of the first paragraph.

The written description rejection is reversed.

2. Obviousness.

We initially note that appellants state that the claims are grouped together for the purposes of this rejection. Appeal Brief, page 5. Accordingly, we shall decide the issues raised in the Examiner's obviousness rejection as they pertain to claim 25. 37 CFR § 1.192(c)(7). We also note that the two Nishi references relied upon by the examiner appear to be the same. Thus, we shall consider the merits of the examiner's rejection as it is based upon Nishi '713.

Claim 25 is directed to a method for detecting a target polynucleotide said to comprise the polynucleotide of claim 7 in a sample. To this end, a sample is hybridized with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample. The probe will specifically hybridize to the target polynucleotide, if present, forming a hybridization complex. The presence or absence of the hybridization complex is an indication as to whether the sample contained the target polynucleotide.

The examiner has determined without dispute by appellants that Nishi '713 describes a polynucleotide encoding a carbohydrate metabolizing enzyme (glutamine:fructose-6-phosphate amidotransferase activity) that is 100% identical to the amino acid sequence set forth in SEQ ID NO:1 of this application. Examiner's Answer, page 6. The examiner has also determined, again without dispute by appellants, that Nishi '713 describes a polynucleotide sequence encoding that polypeptide that is 67.7% identical to the polynucleotide sequence set forth in SEQ ID NO:4 of this application. Id. The basis for the examiner's findings are the sequence comparison printouts

obtained as a result of an electronic search of sequence databases. As seen from the sequence search report dated December 14, 1999, U.S.-09-079-892-4.rng, pages 1-3 the polynucleotide sequence extending from nucleotide 99-2144 of SEQ ID NO:4 of this application is 100% identical to the coding sequence set forth in Nishi '713. See, e.g., Figs. 2A-2F and SEQ ID NO:5 of Nishi '713.

The examiner has concluded that it would have been obvious to a person of ordinary skill in the art to use any 20 contiguous nucleotides in the region of the polynucleotide sequence described in Nishi '713 as a probe in either a hybridization reaction or as part of a set of probes/primers in a PCR reaction to detect a target polynucleotide. Once again, appellants do not dispute this aspect of the examiner's position. Indeed, Nishi suggests as much, stating:

> The DNA encoding the protein or the partial peptide of the present invention can be cloned either by PCR amplification by using synthetic DNA primers having a partial nucleotide sequence of the DNA coding for the protein or by hybridization using the DNA inserted in a suitable vector and labeled DNA fragment or synthetic DNA coding for a part or full region of the protein or the partial peptide of the present invention. The hybridization can be carried out by the method described in Molecular Cloning, 2nd (J. Sambrook et al., Cold Spring Harbor Lab. Press, 1989). When a commercially available DNA library is used, the instructions given in the accompanying manual can be followed.

Nishi '713, column 15, lines 54 through 65.

Where the appellants and the examiner part company in regard to the obviousness rejection has to do with whether claim 25 on appeal is "directed only to detecting the target polynucleotides, comprising the polynucleotides recited in claim [] 7 . . ." (Appeal Brief, page 12) or whether claim 25 is inclusive of "detecting any target polynucleotide which hybridizes to probes generated from the sequence of

Nishi. . .." (Appeal Brief, page 11) (emphasis in each original). Appellants urge that claim 25 must be read such that the claimed method detects only the polynucleotides recited in claim 7. We disagree with appellants' claim construction.

First, appellants' position does not take into account that claim 25 explicitly reads upon a negative result, i.e., the probe comprising at least 20 contiguous nucleotides will not hybridize to any nucleotide sequence in the sample. This is seen in that claim 25 b) includes detecting the absence of a hybridization complex. Since appellants have not contravened the basic premise of the examiner's obviousness rejection, i.e., it would have been obvious to one of ordinary skill in the art to use a probe comprising at least 20 contiguous nucleotides based upon the polynucleotide sequence described in Nishi '713 in a hybridization method, the performance of such a method that results in a negative result reads directly upon claim 25. Thus, the examiner's rejection can be sustained on this basis.

Second, we do not read claim 25 in the manner in which appellants do. In our view, claim 25 is not limited "only to detecting the target polynucleotides comprising the polynucleotides recited in claim [] 7 . . .." Appeal Brief, page 12. Once a probe comprising at least 20 contiguous nucleotides is constructed based upon the polynucleotide sequence described in Nishi '713, the use of that probe in a hybridization method will result in the hybridization complex being formed if the probe hybridizes to any polynucleotide sequence in the sample under the hybridization conditions used. Thus, an appropriately constructed probe based upon the polynucleotide sequence described in Nishi '713 will hybridize to a polynucleotide sequence such as that of Nishi

‘713, that of SEQ ID NO:4 of this application or any other polynucleotide sequence having sufficient complementarity given the hybridization conditions used.

The examiner’s obviousness rejection is affirmed.

The decision of the examiner is affirmed-in-part.

No time period for taking any subsequent action in connection with this appeal may be extended under 37 CFR § 1.136(a).

AFFIRMED-IN-PART

Sherman D. Winters Administrative Patent Judge	)
William F. Smith Administrative Patent Judge	) BOARD OF PATENT) APPEALS AND) INTERFERENCES
Eric Grimes Administrative Patent Judge	)

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